

GenCore version 4.5
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DOM protein - Protein search, using sw model

RUN ON:	March 14, 2002, 17:34:11 ; March 16, 91.4 seconds (wildcard alignments)
	20,827 Million cell updates/sec

Title:	US-09-86-019-7
Perfected score:	69
Sequence:	1 MAMG73H1P05SC 14

Input table: $M=1000 \times 2$
 $\text{Gap}_{\text{row}} = (0, 1)$, $\text{Gap}_{\text{col}} = (0, 5)$

Searches: 47305 sets, 146272329 records
Total number of hits satisfying chosen parameters: 473055

Maximum DB seq	Length:
Maximum DB seq	2000000000

Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

```

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_plant:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mice:*
8: sp_ornitheloc:*
9: sp_phono:*
10: se_flat:*
11: se_fovent:*
12: se_virus:*
13: se_viribacter:*
14: se_mollusci:*

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SUMMARY

Result	No.	Score	Match	Length	DB	15	Description
1	44	62.3	7.2	2	098660	098660	Ornitho urticulobact
2	42	60.9	186	4	090293	090293	Ornitho homo sapien
3	41	59.4	2.44	2	053315	053315	Streptomyces
4	41	59.4	3.0	5	098583	098583	Drosophila
5	41	59.4	5	5	098297	098297	Trypanosoma
6	41	59.4	3.1	10	082416	082416	Papaver somn
7	41	59.4	3.2	5	098642	098642	Streptomyces
8	41	59.4	5.78	5	017444	017444	Drosophila
9	40	58.3	3.30	10	085928	085928	Arabidopsis
10	40	58.3	7.19	10	064794	064794	Arabidopsis
11	40	58.3	1.05	5	094086	094086	Drosophila
12	39	56.5	17.01	15	082322	082322	Arabidopsis
13	38	55.1	1.46	2	087657	087657	Salmonella
14	38	55.1	2.98	2	091381	091381	Pseudomonas
15	38	55.1	4.35	10	091986	091986	Arabidopsis
16	38	55.1	3.45	10	091098	091098	Arabidopsis
17	38	55.1	4.76	3	012618	012618	Artemisia
18	38	55.1	4.76	3	012618	012618	Artemisia
19	38	55.1	5.08	10	082414	082414	Papaver somn

20	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4	1	Q9RMD0	68	55.1	51.8	4	1	4
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Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* on the substrate. The concentration of the spores was 10⁴ spores/g (a), 10⁵ spores/g (b), 10⁶ spores/g (c), 10⁷ spores/g (d), 10⁸ spores/g (e), 10⁹ spores/g (f), 10¹⁰ spores/g (g), 10¹¹ spores/g (h), 10¹² spores/g (i), 10¹³ spores/g (j), 10¹⁴ spores/g (k), 10¹⁵ spores/g (l), 10¹⁶ spores/g (m), 10¹⁷ spores/g (n), 10¹⁸ spores/g (o), 10¹⁹ spores/g (p), 10²⁰ spores/g (q), 10²¹ spores/g (r), 10²² spores/g (s), 10²³ spores/g (t), 10²⁴ spores/g (u), 10²⁵ spores/g (v), 10²⁶ spores/g (w), 10²⁷ spores/g (x), 10²⁸ spores/g (y), 10²⁹ spores/g (z), 10³⁰ spores/g (aa), 10³¹ spores/g (ab), 10³² spores/g (ac), 10³³ spores/g (ad), 10³⁴ spores/g (ae), 10³⁵ spores/g (af), 10³⁶ spores/g (ag), 10³⁷ spores/g (ah), 10³⁸ spores/g (ai), 10³⁹ spores/g (aj), 10⁴⁰ spores/g (ak), 10⁴¹ spores/g (al), 10⁴² spores/g (am), 10⁴³ spores/g (an), 10⁴⁴ spores/g (ao), 10⁴⁵ spores/g (ap), 10⁴⁶ spores/g (aq), 10⁴⁷ spores/g (ar), 10⁴⁸ spores/g (as), 10⁴⁹ spores/g (at), 10⁵⁰ spores/g (au), 10⁵¹ spores/g (av), 10⁵² spores/g (aw), 10⁵³ spores/g (ax), 10⁵⁴ spores/g (ay), 10⁵⁵ spores/g (az), 10⁵⁶ spores/g (ba), 10⁵⁷ spores/g (bb), 10⁵⁸ spores/g (bc), 10⁵⁹ spores/g (bd), 10⁶⁰ spores/g (be), 10⁶¹ spores/g (bf), 10⁶² spores/g (bg), 10⁶³ spores/g (bh), 10⁶⁴ spores/g (bi), 10⁶⁵ spores/g (bj), 10⁶⁶ spores/g (bk), 10⁶⁷ spores/g (bl), 10⁶⁸ spores/g (bm), 10⁶⁹ spores/g (bn), 10⁷⁰ spores/g (bo), 10⁷¹ spores/g (bp), 10⁷² spores/g (bq), 10⁷³ spores/g (br), 10⁷⁴ spores/g (bs), 10⁷⁵ spores/g (bt), 10⁷⁶ spores/g (bu), 10⁷⁷ spores/g (bv), 10⁷⁸ spores/g (bw), 10⁷⁹ spores/g (bx), 10⁸⁰ spores/g (by), 10⁸¹ spores/g (bz), 10⁸² spores/g (ca), 10⁸³ spores/g (cb), 10⁸⁴ spores/g (cc), 10⁸⁵ spores/g (cd), 10⁸⁶ spores/g (ce), 10⁸⁷ spores/g (cf), 10⁸⁸ spores/g (cg), 10⁸⁹ spores/g (ch), 10⁹⁰ spores/g (ci), 10⁹¹ spores/g (cj), 10⁹² spores/g (ck), 10⁹³ spores/g (cl), 10⁹⁴ spores/g (cm), 10⁹⁵ spores/g (cn), 10⁹⁶ spores/g (co), 10⁹⁷ spores/g (cp), 10⁹⁸ spores/g (cq), 10⁹⁹ spores/g (cr), 10¹⁰⁰ spores/g (cs), 10¹⁰¹ spores/g (ct), 10¹⁰² spores/g (cu), 10¹⁰³ spores/g (cv), 10¹⁰⁴ spores/g (cw), 10¹⁰⁵ spores/g (cx), 10¹⁰⁶ spores/g (cy), 10¹⁰⁷ spores/g (cz), 10¹⁰⁸ spores/g (da), 10¹⁰⁹ spores/g (db), 10¹¹⁰ spores/g (dc), 10¹¹¹ spores/g (dd), 10¹¹² spores/g (de), 10¹¹³ spores/g (df), 10¹¹⁴ spores/g (dg), 10¹¹⁵ spores/g (dh), 10¹¹⁶ spores/g (di), 10¹¹⁷ spores/g (dj), 10¹¹⁸ spores/g (dk), 10¹¹⁹ spores/g (dl), 10¹²⁰ spores/g (dm), 10¹²¹ spores/g (dn), 10¹²² spores/g (do), 10¹²³ spores/g (dp), 10¹²⁴ spores/g (dq), 10¹²⁵ spores/g (dr), 10¹²⁶ spores/g (ds), 10¹²⁷ spores/g (dt), 10¹²⁸ spores/g (du), 10¹²⁹ spores/g (dv), 10¹³⁰ spores/g (dw), 10¹³¹ spores/g (dx), 10¹³² spores/g (dy), 10¹³³ spores/g (dz), 10¹³⁴ spores/g (ea), 10¹³⁵ spores/g (eb), 10¹³⁶ spores/g (ec), 10¹³⁷ spores/g (ed), 10¹³⁸ spores/g (ee), 10¹³⁹ spores/g (ef), 10¹⁴⁰ spores/g (eg), 10¹⁴¹ spores/g (eh), 10¹⁴² spores/g (ei), 10¹⁴³ spores/g (ej), 10¹⁴⁴ spores/g (ek), 10¹⁴⁵ spores/g (el), 10¹⁴⁶ spores/g (em), 10¹⁴⁷ spores/g (en), 10¹⁴⁸ spores/g (eo), 10¹⁴⁹ spores/g (ep), 10¹⁵⁰ spores/g (eq), 10¹⁵¹ spores/g (er), 10¹⁵² spores/g (es), 10¹⁵³ spores/g (et), 10¹⁵⁴ spores/g (eu), 10¹⁵⁵ spores/g (ev), 10¹⁵⁶ spores/g (ew), 10¹⁵⁷ spores/g (ex), 10¹⁵⁸ spores/g (ey), 10¹⁵⁹ spores/g (ez), 10¹⁶⁰ spores/g (fa), 10¹⁶¹ spores/g (fb), 10¹⁶² spores/g (fc), 10¹⁶³ spores/g (fd), 10¹⁶⁴ spores/g (fe), 10¹⁶⁵ spores/g (ff), 10¹⁶⁶ spores/g (fg), 10¹⁶⁷ spores/g (fh), 10¹⁶⁸ spores/g (fi), 10¹⁶⁹ spores/g (fj), 10¹⁷⁰ spores/g (fk), 10¹⁷¹ spores/g (fl), 10¹⁷² spores/g (fm), 10¹⁷³ spores/g (fn), 10¹⁷⁴ spores/g (fo), 10¹⁷⁵ spores/g (fp), 10¹⁷⁶ spores/g (fq), 10¹⁷⁷ spores/g (fr), 10¹⁷⁸ spores/g (fs), 10¹⁷⁹ spores/g (ft), 10¹⁸⁰ spores/g (fu), 10¹⁸¹ spores/g (fv), 10¹⁸² spores/g (fw), 10¹⁸³ spores/g (fx), 10¹⁸⁴ spores/g (fy), 10¹⁸⁵ spores/g (fz), 10¹⁸⁶ spores/g (ga), 10¹⁸⁷ spores/g (gb), 10¹⁸⁸ spores/g (gc), 10¹⁸⁹ spores/g (gd), 10¹⁹⁰ spores/g (ge), 10¹⁹¹ spores/g (gf), 10¹⁹² spores/g (gg), 10¹⁹³ spores/g (gh), 10¹⁹⁴ spores/g (gi), 10¹⁹⁵ spores/g (gj), 10¹⁹⁶ spores/g (gk), 10¹⁹⁷ spores/g (gl), 10¹⁹⁸ spores/g (gm), 10¹⁹⁹ spores/g (gn), 10²⁰⁰ spores/g (go), 10²⁰¹ spores/g (gp), 10²⁰² spores/g (gq), 10²⁰³ spores/g (gr), 10²⁰⁴ spores/g (gs), 10²⁰⁵ spores/g (gt), 10²⁰⁶ spores/g (gu), 10²⁰⁷ spores/g (gv), 10²⁰⁸ spores/g (gw), 10²⁰⁹ spores/g (gx), 10²¹⁰ spores/g (gy), 10²¹¹ spores/g (gz), 10²¹² spores/g (ha), 10²¹³ spores/g (hb), 10²¹⁴ spores/g (hc), 10²¹⁵ spores/g (hd), 10²¹⁶ spores/g (he), 10²¹⁷ spores/g (hf), 10²¹⁸ spores/g (hg), 10²¹⁹ spores/g (hh), 10²²⁰ spores/g (hi), 10²²¹ spores/g (hj), 10²²² spores/g (hk), 10²²³ spores/g (hl), 10²²⁴ spores/g (hm), 10²²⁵ spores/g (hn), 10²²⁶ spores/g (ho), 10²²⁷ spores/g (hp), 10²²⁸ spores/g (hq), 10²²⁹ spores/g (hr), 10²³⁰ spores/g (hs), 10²³¹ spores/g (ht), 10²³² spores/g (hu), 10²³³ spores/g (hv

FOR PROSPECTED RECONSTRUCTION	PSO068; R10NFMAL, S.C. 2; 1.
SU SEQUENCE	440 AN; 4747 MW; 2B76.75084614H664 CPO6.62

DB 309 G38R03SCC 305

RESULT 5

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